

Application 10/782,435

RuvB Polynucleotides and Uses Thereof

Analysis of SEQ ID NO: 4 performed using the HmmerPfam program in the GCG suite of sequence analysis programs.

Query: 1121SID4 from: 1 to: 455 WPDEF Case 1121 SEQ ID NO: 4 RuvB

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
TIP49	TIP49 C-terminus	737.6	5.5e-218	1
AAA	ATPase family associated with vario	-22.2	0.15	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
TIP49	1/1	117	439	1	326	737.6	5.5e-218

Alignments of top-scoring domains:

TIP49: domain 1 of 1, from 117 to 439: score 737.6, E = 5.5e-218

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*->RkAIGvRIKEEkeVyEGEVVeleieeaenplgsygtikhgkitLKT
R+AIG+RIKE keVyEGEV+el++eeae+ g+y+k i+h++i LKT
1121SID4 117 RRAIGLRIVENKEVYEGEVTLSPEEAESTTGGYAKSISHVILSLKT 163

tkmektlkLgpkiyEqLqKEkVeaGDVIyIekntGkVkkLGRSdarakdF
+k++k+lKl+++iy++L KEkV +GDVIyIe+n+G+Vk++GR+d a+++
1121SID4 164 VKGTKQLKLDSSIIYDALIKEKVAVGDDVIYIEANSGAVKRVGRCDSPATEY 213

DlmGeadeFvPlPkGEVhKrKEvVqtVTLHDlDvaNARpqGglDlSmmg
Dl ea+e+Vp+PkGEVhK+KE+Vq+VTLHDlD+ana+pqGg+D+ls+mg
1121SID4 214 DL--EAEYVPIPKGEVHKKEIVQDVTLHDLDANAQPOGGQDILSLMG 261

aLfspkktEItDelReeINKkVnkwiEeGkAEIVPGVLFIDEVHMLDIEC
++++p+ktEIt++lR+eINK+Vn++i+eG+AE+VPGVLFIDEVHMLDIEC
1121SID4 262 QMKPRKTEITEKLRQEINKVNVRYIDEGIAELVPGVLFIDEVHMLDIEC 311

FsFLNRALESelAPivilATNRGittIRGTediksPHGIPldLLDRILII
Fs+LNRALES+1+PivilATNRGi+++RGT D sPHGIP+DLLDRl+II
1121SID4 312 PSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIPVDLLDRlVII 360

tTepYteeEIkkiLEiRaqeEgvelseeAldlltkiGeetsSLRYaiqLLt
+Te Y + E+ +IL+iRaq+E++++ee l +L +iG +tSLR aiqL+
1121SID4 361 RTETYGPTEMIQILAIRAQVEEIDMDEESLAYLGEIGQQTSLRHAIQLIS 410

pasilAkkrggkeVeveDVerayeLF1Da<+
pas+++k++g++++ + D e+++ L 1Da
1121SID4 411 PASVVSKTNGREKICKADLEEVSGLYLDA 439

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Appendix C2